SEQUENCE LISTING

<110> Rijksuniversiteit Leiden

<120> method of modulating metabolite biosynthesis in
      recombinant cells

<130> BO 43339

<140> PCT
<141> 2000-07-02

<160> 21

<170> PatentIn Ver. 2.1

<210> 1
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<212> DNA
<213> Catharanthus roseus

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Lys Gly Cys Met Lys Gly Lys Gly Gly Pro Glu Asn Ser His Cys Lys
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         Gly Pro Cys Ala Arg Leu Asn Leu Pro Asn Tyr Arg Ala Ser Glu Glu
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  15     Ser Ser Ser Leu Pro Thr Thr Ser Gly Ser Asp Thr Thr Thr Ala Ser
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         Gly Ile Ser Glu Val Ser Val Tyr Glu Asp Lys Lys Phe Thr Pro Val
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                     180                 185                 190

         Asp Ser Lys Pro Gln Leu Leu Val Asp Ala Gly Thr Pro Met Ser Ala
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         Val Lys Glu Glu Pro Lys Glu Tyr Gln Val Met Asp Ser Gln Ser Glu
             210                 215                 220

  30     Gly Gln Phe Gly Asp Glu Glu Pro Pro Ser Lys Leu Val Cys Lys Glu
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         Val Asp Phe Gly Gln Asp Gln Ala Val Val Pro Ala Val Lys Asn Ala
                         245                 250                 255

  35     Glu Glu Met Gly Gly Glu Met Gly Gly Asp Ile Leu Lys Gly Cys Ser
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         Leu Ser Glu Met Phe Asp Val Asp Glu Leu Leu Ser Val Leu Asp Ser
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         Thr Pro Leu His Ala Ser Asp Phe Gln His Gly Met Gly Asn Gly Asn
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  45     Val Lys Ala Glu Ala Ala Tyr Asn Tyr Ala Pro Ser Trp Asp Ser Ala
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         Phe Gln Leu Gln Asn Gln Asp Pro Lys Leu Gly Ser Gln Gln His Met
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        Ile Ser Pro Asn Tyr Ala Ser Glu Asp Leu Ser Asp Ile Ile Leu Thr
             65                  70                  75                  80

        Asp Ile Phe Lys Asp Gln Asp Asn Tyr Glu Asp Glu Val Val Ala Gly
  25                     85                  90                  95

        Glu Gln Glu Glu Glu Leu Ile Thr Thr Pro Thr Ser Arg Gly Gly Gly
                     100                 105                 110

  30    Gly Gly Gly Cys Glu Gln Arg Ser Asn Glu Glu Trp Ile Arg Tyr Arg
                     115                 120                 125

        Gly Val Arg Arg Arg Pro Trp Gly Lys Phe Ala Ala Glu Ile Arg Asp
             130                 135                 140
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        Pro Lys Arg Lys Gly Ser Arg Ile Trp Leu Gly Thr Tyr Glu Thr Ala
        145                 150                 155                 160

        Glu Asp Ala Ala Leu Ala Phe Asp Gln Ala Ala Phe Gln Leu Arg Gly
  40                     165                 170                 175

        Ser Arg Ala Arg Leu Asn Phe Pro Asn Leu Ile Gly Ser Ala Asn Ala
                     180                 185                 190

        Pro Val Arg Val Ser Pro Arg Arg Arg Ser Ser Ser Cys His Leu Arg
  45                 195                 200                 205

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         Asn Trp Ser Gly Ser Glu Ile Gln Lys Arg Gly Ser Pro Ser Ser Glu
   10          50                   55                   60

         Ser Cys Gln Ser Asn Ser Met Ala Glu Ser Cys Gln Glu Asp Ser Val
             65                   70                   75                   80

   15   Val Gly Thr Pro Pro Glu Ala Ala Ala Gly Gly Gly Cys Ser Lys Asp
                      85                   90                   95

         Trp Asn Arg Tyr Lys Gly Val Arg Arg Arg Pro Trp Gly Lys Phe Ala
                     100                  105                  110
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         Ala Glu Ile Arg Asp Pro Lys Lys Lys Gly Ser Arg Ile Trp Leu Gly
                     115                  120                  125

         Thr Tyr Glu Thr Pro Glu Asp Ala Ala Leu Ala Tyr Asp Ala Ala Ala
   25        130                  135                  140

         Phe Asn Met Arg Gly Ala Lys Ala Arg Leu Asn Phe Pro His Leu Ile
         145                  150                  155                  160

   30   Gly Ser Asn Ile Ser Gly Pro Val Arg Val Asn Pro Arg Lys Arg Phe
                     165                  170                  175

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SEQUENCE LISTING

<110> Rijksuniversiteit Leiden

<120> method of modulating metabolite biosynthesis in
      recombinant cells

<130> BO 43339

<140> PCT
<141> 2000-07-02

<160> 21

<170> PatentIn Ver. 2.1

<210> 1
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            20                  25                  30


Ala Glu Thr Leu Ala Lys Trp Lys Glu Tyr Asn Glu Lys Leu Asp Ala
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Leu Asp Gly Gly Lys Pro Ala Arg Lys Val Pro Ala Lys Gly Ser Lys
    50                  55                  60


Lys Gly Cys Met Lys Gly Lys Gly Gly Pro Glu Asn Ser His Cys Lys
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                    100             105                 110

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 25             195                 200                 205

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                    245                 250                 255
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                290                 295                 300

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Met Tyr Gln Ser Asn Ala His Asn Ser Asp His Leu Thr Phe Leu Pro
 1               5                  10                  15

Pro Leu Val Asp Tyr Gln Phe Leu Asn Asn Asp Phe Asp Phe Ser Glu
            20                  25                  30

Ile Phe Thr Asp Phe Asn Tyr Ala Asn Tyr Asn Tyr Asn Thr Ser Thr
        35                  40                  45

Ser Asp Asn Phe Ser Gly Phe Gln Phe Asn Glu Asn Cys Glu Glu Ile
    50                  55                  60

Ile Ser Pro Asn Tyr Ala Ser Glu Asp Leu Ser Asp Ile Ile Leu Thr
 65              70                  75                      80

Asp Ile Phe Lys Asp Gln Asp Asn Tyr Glu Asp Glu Val Val Ala Gly
            85                  90                      95

Glu Gln Glu Glu Glu Leu Ile Thr Thr Pro Thr Ser Arg Gly Gly Gly
            100                 105                 110

Gly Gly Gly Cys Glu Gln Arg Ser Asn Glu Glu Trp Ile Arg Tyr Arg
        115                 120                 125

Gly Val Arg Arg Arg Pro Trp Gly Lys Phe Ala Ala Glu Ile Arg Asp
    130                 135                 140

Pro Lys Arg Lys Gly Ser Arg Ile Trp Leu Gly Thr Tyr Glu Thr Ala
145                 150                 155                 160

Glu Asp Ala Ala Leu Ala Phe Asp Gln Ala Ala Phe Gln Leu Arg Gly
                165                 170                 175

Ser Arg Ala Arg Leu Asn Phe Pro Asn Leu Ile Gly Ser Ala Asn Ala
            180                 185                 190

Pro Val Arg Val Ser Pro Arg Arg Arg Ser Ser Ser Cys His Leu Arg
        195                 200                 205

Pro Gln
    210
```

<210> 6
<211> 203
<212> PRT
<213> Catharanthus roseus

<400> 6

```
Met Ser Glu Glu Ile Ile Ser Val Ser Asp Arg Phe Leu Leu Ser Leu
```

```
        1                    5                    10                   15

    Ile Glu Glu His Leu Leu Ser Asp Asn Ser Asp Asp Ser Ser Ser Glu
                  20                  25              30
 5
    Leu Thr Ser Thr Glu Glu Asn Trp Glu Glu Ile Phe Ala Asp Phe Leu
              35                  40                  45

    Asn Trp Ser Gly Ser Glu Ile Gln Lys Arg Gly Ser Pro Ser Ser Glu
10          50                  55                  60

    Ser Cys Gln Ser Asn Ser Met Ala Glu Ser Cys Gln Glu Asp Ser Val
        65                  70                  75                  80

15  Val Gly Thr Pro Pro Glu Ala Ala Ala Gly Gly Gly Cys Ser Lys Asp
                      85                  90                  95

    Trp Asn Arg Tyr Lys Gly Val Arg Arg Arg Pro Trp Gly Lys Phe Ala
                  100                 105                 110
20
    Ala Glu Ile Arg Asp Pro Lys Lys Lys Gly Ser Arg Ile Trp Leu Gly
              115                 120                 125

    Thr Tyr Glu Thr Pro Glu Asp Ala Ala Leu Ala Tyr Asp Ala Ala Ala
25      130                 135                 140

    Phe Asn Met Arg Gly Ala Lys Ala Arg Leu Asn Phe Pro His Leu Ile
    145                 150                 155                 160

30  Gly Ser Asn Ile Ser Gly Pro Val Arg Val Asn Pro Arg Lys Arg Phe
                  165                 .170                175

    Pro Ala Glu Pro Ser Thr Thr Ser Ser Ser Ser Ser Ser Ser Ser Ser
              180                 185                 190

35
    Glu Asn Ser Gly Gly Arg Lys Lys Arg Arg Tyr
              195                 200
```

```
40
    <210> 7
    <211> 48
    <212> DNA
    <213> Catharanthus roseus
45
    <400> 7
    gtacatcact cttagaccgc cttctttgaa agtgatttcc cttggacc            48


50  <210> 8
    <211> 25
    <212> DNA
    <213> Artificial Sequence

55  <220>
    <223> Description of Artificial Sequence: primer

    <400> 8
    ccacgtggtt gtagtctctt agacc                                     25
```

```
     <210> 9
     <211> 25
 5   <212> DNA
     <213> Artificial Sequence

     <220>
     <223> Description of Artificial Sequence: primer
10
     <400> 9
     ggtacatcag agaatgaccg ccttc                                    25


15   <210> 10
     <211> 26
     <212> DNA
     <213> Artificial Sequence

20   <220>
     <223> Description of Artificial Sequence: primer

     <400> 10
     cactcttact ggcgcttctt tgaaag                                   26
25

     <210> 11
     <211> 21
     <212> DNA
30   <213> Artificial Sequence

     <220>
     <223> Description of Artificial Sequence: primer

35   <400> 11
     agaccgcgaa gaatgaaagt g                                        21


     <210> 12
40   <211> 29
     <212> DNA
     <213> Artificial Sequence

     <220>
45   <223> Description of Artificial Sequence: primer

     <400> 12
     agaccgcctt cttactttct gatttcccc                                29

50
     <210> 13
     <211> 22
     <212> DNA
     <213> Artificial Sequence
55
     <220>
     <223> Description of Artificial Sequence: primer

     <400> 13
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ttgaaagact aaacccttgg ac                                          22


        <210> 14
   5    <211> 24
        <212> DNA
        <213> Artificial Sequence

        <220>
  10    <223> Description of Artificial Sequence: primer

        <400> 14
        gaaagtgatt tgggaacgac cttg                                 24

  15
        <210> 15
        <211> 22
        <212> DNA
        <213> Artificial Sequence
  20
        <220>
        <223> Description of Artificial Sequence: primer

        <400> 15
  25    cccttgctgg aagtttggtg ag                                   22


        <210> 16
        <211> 21
  30    <212> DNA
        <213> Artificial Sequence

        <220>
        <223> Description of Artificial Sequence: primer
  35
        <400> 16
        ccccaccaaa cccaaaaaaa g                                    21


  40    <210> 17
        <211> 22
        <212> DNA
        <213> Artificial Sequence

  45    <220>
        <223> Description of Artificial Sequence: primer

        <400> 17
        ccatatcctc gatccttttc tc                                   22
  50

        <210> 18
        <211> 34
        <212> DNA
  55    <213> Artificial Sequence

        <220>
        <223> Description of Artificial Sequence: primer
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<400> 18
gaattcatat ggcggaaagc tgtcaggagg attc                                    34


<210> 19
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 19
cgacgtcgta gaaggctccg caggg                                             25


<210> 20
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 20
agatctcata gttccgaaga aatcatttcc gtctcag                                 37


<210> 21
<211> 41
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 21
agactcgtga acttttttgg atataaaatt ttgtacattc c                           41
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